IN THE CLAIMS:

Please amend the claims as follows. A marked-up copy showing the changes made thereto, is attached.

1. (Unchanged From Prior Version) An isolated nucleic acid consisting of a member selected from the group consisting of (a) SEQ ID NOS. 1-8 and 9, (b) complementary base sequences of (a), (c) a mutation of (a) or (b) which is a modified sequence capable of hybridizing at 55°C with SEQ ID NOS. 1-8 and 9 and (d) complementary base sequences of said modified sequences (c).

2. (Twice Amended) A nucleic acid fragment that can be utilized as a primer or probe comprising the nucleic acid according to claim 1.

3. (Unchanged From Prior Version) The isolated nucleic acid according to claim 1, wherein the mutation is partial deletion of the base sequence, addition of an extra base or base sequence, or substitution of bases or partial sequence in the base sequence with other base or base sequence, or a combination thereof.

4. (Unchanged From Prior Version) The nucleic acid fragment according to claim 2, wherein the mutation is partial deletion of the base sequence, addition of an extra base or base sequence, or substitution of bases or partial sequence in the base sequence with other base or base sequence, or a combination thereof.

5. (Twice Amended) A primer comprising a nucleic acid fragment that can be utilized as a primer according to any one of claims 2, 3 or 4, in which, as an additional modification, a marker and/or a moiety, which is attached to a solid-phase carrier, is bound to said nucleic acid fragment.

6. (Twice Amended) A probe comprising a nucleic acid fragment that can be utilized as a probe according to any one of claims 2, 3 or 4, in which, as an additional modification, a marker and/or a moiety, which is attached to a solid-phase carrier is bound to said nucleic acid fragment.

7. (Twice Amended) A primer comprising a combination of two different nucleic acid fragments with a substantial difference in their base sequences, wherein at least one of said two different nucleic acid fragments is a nucleic acid fragment for a primer according to claim 5.

8. (Unchanged From Prior Version) The primer according to claim 5, wherein the base sequence of a nucleic acid fragment for said primer is a modified base sequence subjected to a mutation, comprising partial deletion of the base sequence, addition of an extra base or base sequence, or substitution of a base or partial sequence in the base sequence with other base or base sequence, or combination thereof, based on a base sequence shown in SEQ ID NO: 1 to 9 or complementary base sequence thereof.

9. (Twice Amended) The primer according to claim 7, wherein the base sequence of at least one of said two different nucleic acid fragments is a modified base sequence subjected to a mutation, comprising partial deletion of the base sequence, addition of an extra base or base sequence, or substitution of a base or partial sequence in the base sequence with other base or base sequence, or a combination thereof, based on a base sequence shown in SEQ ID NO: 1 to 9 or complementary base sequence thereof.

10. (Three Times Amended) The primer according to claim 5, wherein said marker or moiety is additionally bound to the 5'-terminal side of the nucleic acid fragment.

11. (Three Times Amended) The probe according to claim 6, wherein said marker or moiety is additionally bound to the 5'-terminal side of the nucleic acid fragment.

12. (Twice Amended) The primer according to claim 7, wherein said marker or moiety is additionally bound to the 5'-terminal side of the nucleic acid fragment.

13. (Twice Amended) The primer according to claim 8, wherein said marker or moiety is additionally bound to the 5'-terminal side of the nucleic acid fragment.

14. (Unchanged From Prior Version) The primer according to claim 5, wherein the marker or the moiety bound to a solid-phase carrier is a biotin reside, a 2,4-dinitrophenyl group or a digoxigenin residue.

15. (Unchanged From Prior Version) The primer according to claim 6, wherein the marker or the moiety bound to a solid-phase carrier is a biotin residue, a 2,4-dinitrophenyl group or a digoxigenin residue.

16. (Unchanged From Prior Version) The primer according to claim 7, wherein the marker or the moiety bound to a solid-phase carrier is a biotin residue, a 2,4-dinitrophenyl group or a digoxigenin residue.

17. (Unchanged From Prior Version) The primer according to claim 9, wherein the marker or the moiety bound to a solid-phase carrier is a biotin residue, a 2,4-dinitrophenyl group or a digoxigenin residue.

18. (Unchanged From Prior Version) The primer according to claim 10, wherein the marker or the moiety bound to a solid-phase carrier is a biotin residue, a 2,4-dinitrophenyl group or a digoxigenin residue.

19. (Amended) A method of detecting a PHA synthesizing microorganism, wherein said method uses at least one kind of nucleic acid fragment according to any one of claims 1 to 4 as a probe.

20. (Amended) A method of detecting a polyhydroxyalkanoate synthesizing microorganism, wherein said method uses at least one kind of nucleic acid fragment according to any one of claims 1 to 4 as a primer.

21. (Unchanged From Prior Version) A method of detecting a polyhydroxyalkanoate synthesizing microorganism, wherein said method uses a primer according to claim 5, and comprises the following four steps of:

(1) preparing a sample in which the presence or absence of a PHA synthesizing microorganism is to be detected;

(2) performing a lysis treatment of cells in the sample, if necessary;

(3) adding said primer to the sample and performing an elongation reaction of the primer; and

(4) performing a detecting operation of the elongation reaction products obtained from the step (3), or

said steps (1), (3), and (4), as well as step (2), if necessary, are conducted.

22. (Unchanged From Prior Version) A method of detecting a polyhydroxyalkanoate synthesizing microorganism, wherein said method uses a primer according to claim 7, and comprises the following four steps of:

(1) preparing a sample in which the presence or absence of a PHA synthesizing microorganism is to be detected;

(2) performing a lysis treatment of cells in the sample, if necessary;

(3) adding said primer to the sample and performing an elongation reaction of the primer; and

(4) performing a detecting operation of the elongation reaction products obtained from the step (3), or

said steps (1), (3), and (4), as well as step (2), if necessary, are conducted.

23. (Unchanged From Prior Version) The method of detecting a polyhydroxyalkanoate synthesizing microorganism according to claim 22, wherein said method uses the primer comprising a combination of two kinds of nucleic acid fragments.

24. (Unchanged From Prior Version) The method of detecting a polyhydroxyalkanoate synthesizing microorganism according to claim 21, wherein said elongation reaction of a primer in said adding step (3) is performed by a polymerase chain reaction.

25. (Unchanged From Prior Version) The method of detecting a polyhydroxyalkanoate synthesizing microorganism according to claim 23, wherein said elongation reaction of a primer in step (3) is performed by a polymerase chain reaction.

REMARKS

This application has been carefully reviewed in light of the Office Action dated October 24, 2002. Claims 1 to 25 are in the application, of which Claims 19 to 25 have been withdrawn from consideration pursuant to a Restriction Requirement entered in